

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: July 17, 2003, 16:09:08 ; Search time 32 Seconds

(without alignments)  
1558.231 Million cell updates/sec

Title: US-09-978-309a-74

Perfect score: 1195

Sequence: 1 OEKYDSMVOSLEEDVTAQFES.....KKKQSETKLQEEINKVGLIK 242

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

1: SP archaea: \*  
2: SP bacteria: \*  
3: SP fungi: \*  
4: SP human: \*  
5: SP invertebrate: \*  
6: SP mammal: \*  
7: SP mhc: \*  
8: SP organelle: \*  
9: SP phage: \*  
10: SP plant: \*  
11: SP rodent: \*  
12: SP virus: \*  
13: SP vertebrate: \*  
14: SP unclassified: \*  
15: SP virus: \*  
16: SP bacteriophage: \*  
17: SP archaea: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	917	76.7	836	11	Q8VDR2
2	905.5	75.8	476	11	Q920Z6
3	893	74.7	713	11	Q9WUF7
4	338	28.3	82	6	Q95JG7
5	338	28.3	82	6	Q8SPM2
6	209	17.5	436	4	Q960X7
7	209	17.5	1388	4	Q9NS87
8	193.5	16.2	1944	13	Q9DGM5
9	193	16.2	1388	13	Q91785
10	191	16.0	795	4	Q9H2G7
11	191	16.0	804	4	Q8TC31
12	191	16.0	1410	4	Q14221
13	191	16.0	1411	4	Q15075
14	190	15.9	1690	5	Q44929
15	189.5	15.9	1941	13	Q9DGM4
16	189	15.8	1690	5	Q9VDE5

17	187	15.6	826	13	Q9YHD5	Q9YHD5 rana catesb
18	185.5	15.5	1790	3	Q07380	Q07380 saccharomy
19	183.5	15.4	1937	6	Q9TV62	Q9TV62 sus scrofa
20	182.5	15.3	1929	13	Q98TQ6	Q98TQ6 notothenia
21	182.5	15.3	1935	13	Q90ZES	Q90ZES brachydania
22	182.5	15.3	1940	6	Q9BE41	Q9BE41 bos taurus
23	181.5	15.2	1598	11	Q922D2	Q922D2 mus musculu
24	180.5	15.1	1938	6	Q9BE40	Q9BE40 bos taurus
25	179.5	15.0	1939	13	Q9PY2	Q9PY2 gallus gall
26	179	15.0	1463	5	Q9GYZ0	Q9GYZ0 strongyloce
27	178.5	14.9	692	5	Q967Z0	Q967Z0 dermatophag
28	178.5	14.9	1930	13	Q9DGD5	Q9DGD5 pennaria ar
29	178.5	14.9	1939	6	Q9TV61	Q9TV61 sus scrofa
30	178	14.9	609	17	Q8TXA4	Q8TXA4 methanopyru
31	176.5	14.8	975	13	Q98TQ5	Q98TQ5 notothenia
32	176.5	14.8	1939	6	Q9TV63	Q9TV63 sus scrofa
33	175.5	14.7	746	4	Q9H6N6	Q9H6N6 homo sapien
34	175.5	14.7	1945	6	Q97757	Q97757 fells silve
35	174.5	14.6	1936	13	Q90TF6	Q90TF6 paracitrit
36	174	14.6	549	5	Q9XZV8	Q9XZV8 hydra atten
37	171	14.3	1320	11	Q9JK25	Q9JK25 raltus norv
38	170.5	14.3	1119	13	P87344	P87344 theagra ch
39	170	14.2	1388	11	P70336	P70336 mus musculu
40	169.5	14.2	1938	13	Q91BD7	Q91BD7 seriola dum
41	169	14.1	764	13	Q91411	Q91411 gallus gall
42	169	14.1	752	11	Q90H23	Q90H23 raltus norv
43	169	14.1	806	11	Q8VD04	Q8VD04 mus musculu
44	169	14.1	837	11	Q9JH24	Q9JH24 raltus norv
45	169	14.1	1489	5	Q8T805	Q8T805 drosophila

## ALIGNMENTS

RESULT 1	Q8VDR2	PRELIMINARY:	PRT:	836 AA.
ID	Q8VDR2	Q8VDR2		
AC	Q8VDR2	Q8VDR2		
DT	01-MAR-2002 (TREMBLrel. 20, Created)			
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	Similar to hyaluronan mediated motility receptor (RHAMM).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Strausberg R.			
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: BC021427; AAH21427.1;			
KW	Receptor.			
SO	SEQUENCE	836 AA;	96670 MW;	B9BDDA22EBCE652 CRC64;

Query Match 76.7%; Score 917; DB 11; Length 836;  
Best Local Similarity 76.4%; Pred. No. 1.5e-38;  
Matches 185; Conservative 19; Mismatches 38; Indels 0; Gaps 0;

QY	1	OEKYDSMVOSLEEDVTAQFESKALTSSEITDLENSIOEKAKAKNAEDVOHOLAT 60
DB	568	OEKYNDTPAOSLRVTQLESYKSTLEKEDLENTLOEKVAMAEKSEVEDVOOILTA 627
QY	61	ESSNOEYVRLDLOTKRSALKETKEITVSPFOKITDLONLQKQOEDPRKOLEDEGR 120
DB	628	ESNOEYAVVQLOLRSTLEKEIEITSEFLEKITDLONLQKQOEDPRKOLEDEGR 687
QY	121	KAKEKNTAELTEINKRWLLYEELYNKTRPFOIQDADFVEKQALLNEGAQOELNKI 180
DB	688	TAKEKNTAELTEINKRWLLYEELYNKTRPFOIQDADFVEKQALLNEGAQOELNKI 747
QY	181	RDSYAKLGHONIKKIKHVKIKDENSQKSKVSKRQOLAKKQSEKRLQEEIKVGL 240
DB	748	RDSYAKLGHONIKKIKHVKIKDENSQKSKVSKRQOLAKKQSEKRLQEEIKVGL 807

OY 241 IK 242  
DB 808 IR 809

## RESULT 2

OY 092026 PRELIMINARY; PRT: 476 AA.  
AC 092026;  
DT 01-DEC-2001 (TREMblrel. 19, Created)  
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
DE Hyaluronan receptor.  
OS Mus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10095;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92299690; PubMed=1376732;  
RA Hardwick C., Hoare K., Owens R., Hohn H.P., Hook M., Moore D.,  
RA Cripps V., Austen L., Nance D.M., Turley E.A.;  
RT "Molecular cloning of a novel hyaluronan receptor that mediates tumor  
cell motility."  
RL J. Cell Biol. 117:1343-1350(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92348516; PubMed=1639856;  
RA Hardwick C., Hoare K., Owens R., Hohn H.P., Hook M., Moore D.,  
RA Cripps V., Austen L., Nance D.M., Turley E.A.;  
RT "Correction. Molecular cloning of a novel hyaluronan receptor that  
mediates tumor cell motility."  
RL J. Cell Biol. 118:753-753(1992).  
DR EMBL; S41029; AAA09809.1;  
KM Receptor.  
SQ SEQUENCE 476 AA; 55486 MW; 62DCA82045EE0CB2 CRC64;

Query Match 75.8%; Score 905.5; DB 11; Length 476;  
Best Local Similarity 76.0%; Pred. No. 3e-38;  
Matches 184; Conservative 20; Mismatches 37; Indels 1; Gaps 1;

OY 1 QEKYDSWVOSLEEDVTAOFESYKALTAISEIDKLENSLOEKAKAKNAEDVOHOTLAT 60  
DB 209 QEKYDNTAGSLRVSQLESYKSTLKEIEDKLENTLOEKVAMAEKSEVEDVQOQILTA 268  
OY 61 ESSNOEYVRMLDLQTSALKEITEITVSFLQKTTDLONOLOKQOEDPRKOLEDEGR 120  
DB 269 ESTNOEYARVQDLONRSTLKEIEITSSFLKTTDLONOLOKQOEDPRKOLEDEGR 328  
OY 121 KAKEKNTALTEIINKKRLIYELYNKTRPFOIOLDAFEVEKQALLNEHGAQOELNKT 180  
DB 329 TKEKEVNTALTEIINKKRLIYELYNKTRPFOIOLDAFEVEKQALLNEHGAQOELNKT 387  
OY 181 RDSYAKLLGHONLKQIKHVVRLKDNESQKSEVSKRLQALAKKQSETKLOEELNKVYG 240  
DB 388 RDSYAKLLGHONLKQIKHVVRLKDNESQKSEVSKRLQALAKKQSETKLOEELNKVYG 447  
OY 241 IK 242  
DB 448 IR 449

## RESULT 3

OY 09WU77 PRELIMINARY; PRT: 713 AA.  
AC 09WU77;  
DT 01-NOV-1999 (TREMblrel. 12, Created)  
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)  
DE Hyaluronan receptor RHAMM.  
GN RHAMM.  
OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE DAWLEY;  
RA Li X., Lynn B., Nagy J.L., Cattini P.A.;  
RT "RHAMM cDNA from rat brain."  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PHOCHROMOCYTOMA;  
RA Lynn B.D., Li X., Cattini P.A., Nagy J.L.;  
RT "Sequence, protein expression and erk association of the hyaladherin  
RT RHAMM in PC12 cells."  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF133037; AAD24473.1;  
DR EMBL; AF336825; AAK21904.1;  
KM Receptor.  
SQ SEQUENCE 713 AA; 82395 MW; 2PE310D5759C6CB3 CRC64;

Query Match 74.7%; Score 893; DB 11; Length 713;  
Best Local Similarity 74.0%; Pred. No. 2e-37;  
Matches 179; Conservative 21; Mismatches 42; Indels 0; Gaps 0;

OY 1 QEKYDSWVOSLEEDVTAOFESYKALTAISEIDKLENSLOEKAKAKNAEDVOHOTLAT 60  
DB 442 QEKSDPAOLRLRVTQALLESYKSTLKEIEDKLENTLOEKVAMAEKSEVEDVQOQILTA 501  
OY 61 ESSNOEYVRMLDLQTSALKEITEITVSFLQKTTDLONOLOKQOEDPRKOLEDEGR 120  
DB 502 ESTNOEYARVQDLONRSTLKEIEITSSFLKTTDLONOLOKQOEDPRKOLEDEGR 561  
OY 121 KAKEKNTALTEIINKKRLIYELYNKTRPFOIOLDAFEVEKQALLNEHGAQOELNKT 180  
DB 562 MTKEKAVVTEIINKKRLIYELYNKTRPFOIOLDAFEVEKQALLNEHGAQOELNKT 621  
OY 181 RDSYAKLLGHONLKQIKHVVRLKDNESQKSEVSKRLQALAKKQSETKLOEELNKVYG 240  
DB 622 RDSYAKLLGHONLKQIKHVVRLKDNESQKSEVSKRLQALAKKQSETKLOEELNKVYG 681  
OY 241 IK 242  
DB 682 IR 683

## RESULT 4

OY 095JG7 PRELIMINARY; PRT: 82 AA.  
AC 095JG7;  
DT 01-DEC-2001 (TREMblrel. 19, Created)  
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
DE Hyaluronan acid-mediated motility receptor (Fragmant).  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=TRACHEA;  
RA Aoki T.A., Forteza R.M., Conner G.E.;  
RT "Receptor for hyaluronan acid mediated motility in sheep (Ovis aries)  
RT trachea."  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF10973; AAK69578.1;  
KM Receptor.  
FT NON\_TER.  
SQ SEQUENCE 82 AA; 9452 MW; 46B875555C0F1B66 CRC64;

Query Match 28.3%; Score 338; DB 6; Length 82;

Best Local Similarity 89.5%; Pred. No. 1.3e-10;  
Matches 68; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 167 LNEHGAQEOQLNRDYSYAKILGHONLKOKIKHYVVKLDKNSOLKSEVSKLRQOLAKKKQ 226  
DB 1 LNEHGAQEOQLNRDYSYAKILGHONLKOKIKHYVVKLDKNSOLKSEVSKLRQOLAKKKQ 60

QY 227 SETKLOEELNKVIGIK 242  
DB 61 SEAKLOEELNKVIGIK 76

## RESULT 5

OSPM2 PRELIMINARY; PRT; 82 AA.

AC 08SPM2; 01-JUN-2002 (TREMBLrel. 21, Created)  
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
DE Receptor for hyaluronic acid mediated motility (fragment).  
GN RHAMM.

OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovine; Bos.  
OX NCBI\_TaxID=9913;

RN 11  
RP SEQUENCE FROM N.A.

RC TISSUE=OVARY;

RA Schoenfelder M., Einspanier R.;

RT "Expression of HAS-system during oocyte maturation in the cow."  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; A439694; CAD29126.1; -

FT NON\_TER 1 1

SO SEQUENCE 82 AA; 9452 MW; 46B87555C0F1B66 CRC64;

Query Match 28.3%; Score 338; DB 6; Length 82;  
Best Local Similarity 89.5%; Pred. No. 1.3e-10;

Matches 68; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 167 LNEHGAQEOQLNRDYSYAKILGHONLKOKIKHYVVKLDKNSOLKSEVSKLRQOLAKKKQ 226  
DB 1 LNEHGAQEOQLNRDYSYAKILGHONLKOKIKHYVVKLDKNSOLKSEVSKLRQOLAKKKQ 60

QY 227 SETKLOEELNKVIGIK 242  
DB 61 SEAKLOEELNKVIGIK 76

## RESULT 6

Q96JX7 PRELIMINARY; PRT; 436 AA.

AC 096JX7; 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE CDNA FLJ14910 f1s, clone PLACE1006368, weakly similar to  
DE hyaluronan-mediated motility receptor.  
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;

RN 11  
RP SEQUENCE FROM N.A.

RC TISSUE=PLACENTA;

RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,  
RA Watanabe M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,  
RA Watanabe J., Kimura K., Murakami K., Ishii S., Kawai Y., Sakiguchi S.,  
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,  
RA Niimiya K., Iwayanagi T.;

RT "NEDO human cDNA sequencing project."  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK027816; BAB55389.1; -

SO SEQUENCE 436 AA; 51433 MW; 3BE3ABDB7A7821D CRC64;

Query Match 17.5%; Score 209; DB 4; Length 436;  
Best Local Similarity 24.8%; Pred. No. 0.0018;

Matches 68; Conservative 57; Mismatches 101; Indels 48; Gaps 7;

QY 1 QEKYDSMVOSLEEV-----TAQFESYK-----LTASEIDKLKNSLSQEK 43  
DB 166 KNEYNFMRQLEHVMSAEDPOSPKTPPHQTHLAKLTOTDEIEDGRASSTSEHLV 225

QY 44 AKAGNAEDVOHOLATESSNOEYVRMLDLO---TKSALKETEIKETVSPLOKTDLO 100  
DB 226 TKLNEDEVNAELIRKREKRENTRELSQOLIEKNMLLOGLDDIK---RQKENSQ 282

QY 101 N-----OLKQOEDFRKO-----LEDEGRKAKEKNTVAELTEETINKV 138  
DB 283 NHPDNOOLKNEQESIKERLAKSKIYEMLKMKADLEEVQALYNKMECLRMTEDEVERT 342

QY 139 RLIEELYNKTRFQIOLDAFEVQKALNEHGAQEOQLNRDYSYAKILGHONLKOKIK 198  
DB 343 QTLSEKAFQEKQOLRSLKLEMYERERTSQEMELRKQYCLAENGKLVGHONLHQIK 402

QY 199 HVKLKDENSOLKSEVSKLRQO---LAKKQSEF 229  
DB 403 YVRLKKNVRLAEETEKLAENVFLKEKRSES 436

QY 139 RLIEELYNKTRFQIOLDAFEVQKALNEHGAQEOQLNRDYSYAKILGHONLKOKIK 198  
DB 343 QTLSEKAFQEKQOLRSLKLEMYERERTSQEMELRKQYCLAENGKLVGHONLHQIK 402

QY 199 HVKLKDENSOLKSEVSKLRQO---LAKKQSEF 229  
DB 403 YVRLKKNVRLAEETEKLAENVFLKEKRSES 436

QY 139 RLIEELYNKTRFQIOLDAFEVQKALNEHGAQEOQLNRDYSYAKILGHONLKOKIK 198  
DB 343 QTLSEKAFQEKQOLRSLKLEMYERERTSQEMELRKQYCLAENGKLVGHONLHQIK 402

QY 199 HVKLKDENSOLKSEVSKLRQO---LAKKQSEF 229  
DB 403 YVRLKKNVRLAEETEKLAENVFLKEKRSES 436

QY 139 RLIEELYNKTRFQIOLDAFEVQKALNEHGAQEOQLNRDYSYAKILGHONLKOKIK 198  
DB 343 QTLSEKAFQEKQOLRSLKLEMYERERTSQEMELRKQYCLAENGKLVGHONLHQIK 402

QY 199 HVKLKDENSOLKSEVSKLRQO---LAKKQSEF 229  
DB 403 YVRLKKNVRLAEETEKLAENVFLKEKRSES 436

QY 139 RLIEELYNKTRFQIOLDAFEVQKALNEHGAQEOQLNRDYSYAKILGHONLKOKIK 198  
DB 343 QTLSEKAFQEKQOLRSLKLEMYERERTSQEMELRKQYCLAENGKLVGHONLHQIK 402

QY 199 HVKLKDENSOLKSEVSKLRQO---LAKKQSEF 229  
DB 403 YVRLKKNVRLAEETEKLAENVFLKEKRSES 436

QY 139 RLIEELYNKTRFQIOLDAFEVQKALNEHGAQEOQLNRDYSYAKILGHONLKOKIK 198  
DB 343 QTLSEKAFQEKQOLRSLKLEMYERERTSQEMELRKQYCLAENGKLVGHONLHQIK 402

QY 199 HVKLKDENSOLKSEVSKLRQO---LAKKQSEF 229  
DB 403 YVRLKKNVRLAEETEKLAENVFLKEKRSES 436

QY 139 RLIEELYNKTRFQIOLDAFEVQKALNEHGAQEOQLNRDYSYAKILGHONLKOKIK 198  
DB 343 QTLSEKAFQEKQOLRSLKLEMYERERTSQEMELRKQYCLAENGKLVGHONLHQIK 402

QY 199 HVKLKDENSOLKSEVSKLRQO---LAKKQSEF 229  
DB 403 YVRLKKNVRLAEETEKLAENVFLKEKRSES 436

QY 139 RLIEELYNKTRFQIOLDAFEVQKALNEHGAQEOQLNRDYSYAKILGHONLKOKIK 198  
DB 343 QTLSEKAFQEKQOLRSLKLEMYERERTSQEMELRKQYCLAENGKLVGHONLHQIK 402

QY 199 HVKLKDENSOLKSEVSKLRQO---LAKKQSEF 229  
DB 403 YVRLKKNVRLAEETEKLAENVFLKEKRSES 436

QY 139 RLIEELYNKTRFQIOLDAFEVQKALNEHGAQEOQLNRDYSYAKILGHONLKOKIK 198  
DB 343 QTLSEKAFQEKQOLRSLKLEMYERERTSQEMELRKQYCLAENGKLVGHONLHQIK 402

QY 199 HVKLKDENSOLKSEVSKLRQO---LAKKQSEF 229  
DB 403 YVRLKKNVRLAEETEKLAENVFLKEKRSES 436

QY 139 RLIEELYNKTRFQIOLDAFEVQKALNEHGAQEOQLNRDYSYAKILGHONLKOKIK 198  
DB 343 QTLSEKAFQEKQOLRSLKLEMYERERTSQEMELRKQYCLAENGKLVGHONLHQIK 402

QY 199 HVKLKDENSOLKSEVSKLRQO---LAKKQSEF 229  
DB 403 YVRLKKNVRLAEETEKLAENVFLKEKRSES 436

QY 139 RLIEELYNKTRFQIOLDAFEVQKALNEHGAQEOQLNRDYSYAKILGHONLKOKIK 198  
DB 343 QTLSEKAFQEKQOLRSLKLEMYERERTSQEMELRKQYCLAENGKLVGHONLHQIK 402

QY 199 HVKLKDENSOLKSEVSKLRQO---LAKKQSEF 229  
DB 403 YVRLKKNVRLAEETEKLAENVFLKEKRSES 436

QY 139 RLIEELYNKTRFQIOLDAFEVQKALNEHGAQEOQLNRDYSYAKILGHONLKOKIK 198  
DB 343 QTLSEKAFQEKQOLRSLKLEMYERERTSQEMELRKQYCLAENGKLVGHONLHQIK 402

QY 199 HVKLKDENSOLKSEVSKLRQO---LAKKQSEF 229  
DB 403 YVRLKKNVRLAEETEKLAENVFLKEKRSES 436

QY 139 RLIEELYNKTRFQIOLDAFEVQKALNEHGAQEOQLNRDYSYAKILGHONLKOKIK 198  
DB 343 QTLSEKAFQEKQOLRSLKLEMYERERTSQEMELRKQYCLAENGKLVGHONLHQIK 402

QY 199 HVKLKDENSOLKSEVSKLRQO---LAKKQSEF 229  
DB 403 YVRLKKNVRLAEETEKLAENVFLKEKRSES 436

QY 139 RLIEELYNKTRFQIOLDAFEVQKALNEHGAQEOQLNRDYSYAKILGHONLKOKIK 198  
DB 343 QTLSEKAFQEKQOLRSLKLEMYERERTSQEMELRKQYCLAENGKLVGHONLHQIK 402

Db 1235 NHPDNOJLKEQESIKERLAKSVYEEELKAKADLEFVQSLYNKECECLPMTDEVEET 1294  
 QY 139 RLLYEELYNKTFPFOIOLDAFEVEKQALLNEHGAOEOJLNKIRDSYAKLLGHONLKOKIK 198  
 Db 1295 OFLESKAPQEKOLSKLEEMEYEEERPTSOEWEMLRKQVECLAENGKLVGNONLHOKIO 1354  
 QY 199 HVVKLKDENSOLSKSVSKLRQO---LAKKROSET 229  
 Db 1355 YVVRLLKENVRKLAETEKIRANVFLKKEKRSSES 1388

## RESULT 8

Q9DGM5 PRELIMINARY: PRT: 1944 AA.  
 AC Q9DGM5:  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang Q., Bandman E.  
 RT "Seven skeletal myosin heavy chain genes (MYHC) are organized as a  
 RT multigene complex in the chicken genome."  
 RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF272033; AAF99314.1;  
 DR HSSP; P13538; 2MYS.  
 DR InterPro: IPR000048; 10\_region.  
 DR InterPro: IPR001609; myosin\_head.  
 DR InterPro: IPR004099; myosin\_N.  
 DR InterPro: IPR002928; myosin\_tail.  
 DR InterPro: IPR000533; Tropomyosin.  
 DR Pfam: PF00612; IQ; 1.  
 DR Pfam: PF00063; myosin\_head; 1.  
 DR Pfam: PF02736; myosin\_N; 1.  
 DR Pfam: PF01576; myosin\_tail; 1.  
 DR PRINTS; PRO0193; MIOSINHEAVY.  
 DR PRINTS; PRO0194; TROPOMYOSIN.  
 DR ProDom; PD000355; myosin\_head; 1.  
 DR SMART; SM00015; IQ; 1.  
 DR SMART; SM00242; MYSC; 1.  
 SO SEQUENCE 1944 AA; 223211 MW; 154F438220072D68 CRC64;

Query Match 16.2%; Score 193.5; DB 13; Length 1944;  
 Best Local Similarity 21.3%; Pred. No. 0.044;

Matches 76; Conservative 53; Mismatches 106; Indels 121; Gaps 9;

QY 8 VQSLQEDVTAQFESYKALTAASEIEDLKLQENSLQEKRAAKGNAEDVOHILATSESSNOEY 67  
 Db 1215 IONLQVOKOLKEKSEKMETIDDLASNMESVSKAKANLEKMCRTLEDLSIKTSKEEBH 1274  
 QY 68 VMMLDLQTSALKTELEKEIT-----VSFLQITDLONLKQO--- 106  
 Db 1275 QRMINDLSTORARLQTESGEYSROYEEKDALISQSRGQATQOIEELKRLLEEIRAK 1334  
 QY 107 -----EED-----FRKQLEDEGRKAEKENTTAELTEINKWRLY-----DEL 145  
 Db 1335 NALAHALQARHDCCLLEQYEEEOEAKGELQALSKANSSEVAQWRTRYEDAIQIRTEL 1394  
 QY 146 YNKTFFQIOLD-----AFVEKQALLNE-----HGAQEOJLNKIR 181  
 Db 1395 EEAKKKLAQRLODAEHEVEAVNACASLEKTKQRLQNEVEDLMDVERANACARLDKQ 1454  
 QY 182 DSYAKLLGHONLK-----OKIKHVVLKQENSLK 211  
 Db 1455 KNPKIIIAEMWOKYEETOAELEASQKESRSISTELFKKKNAYEESLDHLTLTKRENKNO 1514

QY 212 SEVSKLRQALAK-----KKO-----SETKQOEELNKLVLGK 242  
 Db 1515 QEISDLTQIAGGCAHIELEKVKQKQIDQEKSEIQALAEAEASLEHEGKTLRIQ 1570

## RESULT 9

Q91785 PRELIMINARY: PRT: 1388 AA.  
 AC Q91785:  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 OS KLP2.  
 CC Xenopus laevis (African clawed frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 CC Xenopodinae; Xenopus.  
 NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bolet H., Karsenti E., Vernos I.  
 RT "Xlp2, a new Xenopus centrosomal kinesin-like protein required for  
 RT centrosome separation during mitosis."  
 RL Cell 0:0-0(0).  
 DR EMBL; X94082; CAA63826.1;  
 DR HSSP; P17119; 3KAR.  
 DR InterPro: IPR001752; kinesin\_motor.  
 DR Pfam: PF00225; kinesin; 1.  
 DR PRINTS; PRO0380; KINESINHEAVY.  
 DR SMART; SM00129; KISC; 1.  
 DR PROSITE; PS00411; KINESIN\_MOTOR\_DOMAIN1; 1.  
 DR PROSITE; PS00667; KINESIN\_MOTOR\_DOMAIN2; 1.  
 KW ATP-binding; Coiled coil; Microtubules; Motor protein.  
 SO SEQUENCE 1388 AA; 159141 MW; 1F882538B9AE28E CRC64;

Query Match 16.2%; Score 193; DB 13; Length 1388;  
 Best Local Similarity 22.9%; Pred. No. 0.034;

Matches 71; Conservative 51; Mismatches 92; Indels 96; Gaps 7;

QY 9 QSLQEDVTAQFESYKALTAASEIEDL-----KLQENSLQEKRAAKGNA 50  
 Db 1079 EELEKLTFAFNQOALHTHEKEVEEQISELTNQVYKMTDLEISRQEKIRASSS 1138  
 QY 51 -----EDVQOILATE-----SSNOEYVMMLDLQTK 77  
 Db 1139 SSPVLPPEPRTPGPNPDSIELANLOKRTNLEILVSEINEERTSKNEIIRL-----K 1192  
 QY 78 SALKTELEKEITVSFLQRT-IDLONLK-----QOEDEFRKQLEDEGRKA 122  
 Db 1193 MOLCETEMRLQIONLQCMCKELKSQLENCNNVNMKSDQRPMDQDKRELEKEYSRIM 1252  
 QY 123 EKENTTA-----ELTEINKWRLYEELYNKTFPFOIOLDA 158  
 Db 1253 EKGKATEIILQALQELQETRNILCTKQSHLWELSEKTEIRTSLSAKAFTEKEEIRSLIEG 1312  
 QY 159 FEVEKQALLNEHGAOEOJLNKIRDSYAKLLGHONLKQIKIRVVLKQENSLKSEVSKLR 218  
 Db 1313 KYEETEKLSHLDMLRKQVFLAENGKIIIGHQPNQKIOYLVKLKKNKALLBEAEKLR 1372  
 QY 219 QQLAKKROSE 228  
 Db 1373 IENFLKESK 1382

## RESULT 10

Q9H2G7 PRELIMINARY: PRT: 795 AA.  
 AC Q9H2G7:  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 CC CTL tumor antigen set-1 (Fragment).

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=21143360; PubMed=11149944;
RA Eichmuller S., Usener D., Dummer R., Stein A., Thiel D.,
RA Schandorf D.,
RT "Serological detection of cutaneous T-cell lymphoma-associated
RT antigens.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:629-634(2001).
DR EMBL: AF273043; AAC34903.1; -.
FT NON-TER 795
SQ SEQUENCE 795 AA; 93500 MW; 45472A86A5A7ADFA CRC64;

Query Match 16.0%; Score 191; DB 4; Length 795;
Best Local Similarity 23.3%; Pred. No. 0.025;
Matches 79; Conservative 53; Mismatches 103; Indels 104; Gaps 12;

QY 1 OEKYSMVOSLEDVTAOFESYKALPTAS---EIEDLK-----LENSLQEKAKAG 47
DB 402 EDQKILTMELQKSSLEEMTKLTNNKEVELELKVGEKETLYENKQF-EKTAEBL 460
QY 48 KNAE-----DVHQIATSSNOEYVRMLDLOTK---SALKETEI----85
DB 461 KCTEOELIGLQAREKEVHDLFIQTAITTSSEQYSEKVEDKTELENEKLTNLTSHC 520
QY 86 -----KETVSFLQKIDLOLQKOEEDFKOLEDEGRAEAKENTTAELTEINRW 138
DB 521 NKLSLENKELT---OETSDMTLELKNQOEDINNNKOEERMLKQIENLOETLOLREL 576
QY 139 RLVEELYNKTKPFOIQLDAFE-----VEQALLNEHGAQEOU 177
DB 577 EYVREELKQKRDVEKCKLDKSEENNNLRQVENNKKYIEELQOEKALKKGTASQOL 636
QY 178 N-----KIRDSYA-----KLGHONLKOKIKHVYKLDENSOLK 211
DB 637 NYVEIKVKNLELELESARKQFGEITDTYQKEIEDKISEENLLEVEKAKVIADENVKIQ 696
QY 212 SEVSKLRQ-----LAKKQSETKLOEELNKVIGI 241
DB 697 KEIDK-RCQHKIAEMVAMEKHKHQYDKIIEERDSEGL 734

RESULT 11
O8RC31
ID 08TC31; PRELIMINARY; PRT; 804 AA.
AC 08TC31;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DR 01-JUN-2002 (Tremblrel. 21, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Similar to synaptonemal complex protein 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC026162; AAH26162.1; -.
FT NON-TER 804 AA; 94504 MW; C7A6FAB55989CEAS CRC64;

Query Match 16.0%; Score 191; DB 4; Length 804;
Best Local Similarity 23.3%; Pred. No. 0.025;
Matches 79; Conservative 53; Mismatches 103; Indels 104; Gaps 12;

QY 1 OEKYSMVOSLEDVTAOFESYKALPTAS---EIEDLK-----LENSLQEKAKAG 47
DB 402 EDQKILTMELQKSSLEEMTKLTNNKEVELELKVGEKETLYENKQF-EKTAEBL 460

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QY 48 KNAE-----DVHQIATSSNOEYVRMLDLOTK---SALKETEI----85
DB 461 KCTEOELIGLQAREKEVHDLFIQTAITTSSEQYSEKVEDKTELENEKLTNLTSHC 520
QY 86 -----KETVSFLQKIDLOLQKOEEDFKOLEDEGRAEAKENTTAELTEINRW 138
DB 521 NKLSLENKELT---OETSDMTLELKNQOEDINNNKOEERMLKQIENLOETLOLREL 576
QY 139 RLVEELYNKTKPFOIQLDAFE-----VEQALLNEHGAQEOU 177
DB 577 EYVREELKQKRDVEKCKLDKSEENNNLRQVENNKKYIEELQOEKALKKGTASQOL 636
QY 178 N-----KIRDSYA-----KLGHONLKOKIKHVYKLDENSOLK 211
DB 637 NYVEIKVKNLELELESARKQFGEITDTYQKEIEDKISEENLLEVEKAKVIADENVKIQ 696
QY 212 SEVSKLRQ-----LAKKQSETKLOEELNKVIGI 241
DB 697 KEIDK-RCQHKIAEMVAMEKHKHQYDKIIEERDSEGL 734

RESULT 12
O14221
ID 014221; PRELIMINARY; PRT; 1410 AA.
AC 014221;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, last annotation update)
DE Endosome-associated protein.
GN EEA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95286647; PubMed=7768953;
RA Mu F.T., Callaghan J.M., Steele-Mortimer O., Stenmark H., Patton R.G.,
RA Campbell P.L., McCluskey J., Yeo J.P., Tock E.P., Toh B.H.,
RT "EEA1, an early endosome-associated protein. EEA1 is a conserved
RT alpha-helical peripheral membrane protein flanked by cysteine
RT 'fingers' and contains a calmodulin-binding IQ motif.";
RL J. Biol. Chem. 270:13503-13511(1995).
DR EMBL: LA0157; AAA79121.1; -.
DR InterPro: IPR000822; Znf_C2H2.
DR InterPro: IPR000306; Znf_FYVE.
DR Pfam: PF01363; FYVE; 1.
DR SMART: SM00064; FYVE; 1.
DR SMART: SM00355; Znf_C2H2; 1.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
DR PROSITE: PS0157; ZINC_FINGER_C2H2_2; 1.
KW DNA-binding; Zinc-finger.
SQ SEQUENCE 1410 AA; 162496 MW; DFOF9464D70A8AD CRC64;

Query Match 16.0%; Score 191; DB 4; Length 1410;
Best Local Similarity 27.7%; Pred. No. 0.043;
Matches 74; Conservative 50; Mismatches 69; Indels 74; Gaps 12;

QY 1 OEKYSMVOSLEDVTAOFESYKALPTASIEDTKLENSLQEKAKAGNAEDVHQ-----56
DB 715 KEKYSLSQKTELELGQIK-----KLEADSLVYKASKE-QALDDLOQROLN 760
QY 57 -----ILATESSNO-----EYVRML-LDLOTSALKETEKEITVSFLQKIDLOLQKQ 106
DB 761 TDLELRATELSQKLEMEKEIVSTRDLQKKS-----PALESIKQKLT-----KOE 806
QY 107 EEDFKOLEDEGRAEAKENTTAELTEINRWLYEELYNKTKPFOIQLDAFEVKEKAL 166
DB 807 EE---KQILKODEFELSOET-----KIQHEELNNNIQTVTTELQKVKNEKAL 851
QY 167 LNEHGAQEOUINKTRDSY-----AKLGHONLKOKIKHVYKLDENSOLK 211

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Db 852 MTELSTVVKDLKSLVSDSLNKSSEFEKNGKRAILDEKTEKELKHOLQVOMENT-LK 910  
 QY 212 SEVSKRLQCLAKKQSETKLOEELNKV 238  
 Db 911 -FOKELKSLKEKEKESHOLKLELNSM 936

## RESULT 13

ID Q15075 PRELIMINARY; PRT: 1411 AA.  
 AC Q15075;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 GN Endosomal protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Seelig H.P.  
 RL Submitted (Apr-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: X78998; CA55632.1;  
 DR InterPro: IPR000822; Znf\_C2H2.  
 DR InterPro: IPR000306; Znf\_FYVE.  
 DR Pfam: PF01363; FYVE; 1.  
 DR SMART: SM00064; FYVE; 1.  
 DR SMART: SM00355; Znf\_C2H2; 1.  
 DR PROSITE: PS00028; ZINC\_FINGER\_C2H2\_1; UNKNOWN\_1.  
 DR PROSITE: PS0157; ZINC\_FINGER\_C2H2\_2; 1.  
 DR DNA-binding; Zinc-finger.  
 KW SEQUENCE 1411 AA; 162465 MW; C3B1777FE34B6D CRC64;  
 SQ

Query Match 16.0%; Score 191; DB 4; Length 1411;  
 Best Local Similarity 27.7%; Pred. No. 0.043;  
 Matches 74; Conservative 50; Mismatches 69; Indels 74; Gaps 12;

QY 1 QERYDSVQSLQEDVTAQFESYKALTYSEIDKLKLENSLOEKAKGNADVOHQ-----56  
 Db 715 KERYLSLEKTEELLEGQIK-----KLEADSLVSKSKQ-OLADLOOQROIN 760  
 QY 57 -----ILATESNC-----EYRML-IDLOTKSLKTEKEITVSELOKTTDLONLQKQ 106  
 Db 761 TDELFATLSTKOLEMEKEKIVSSTRDLQKKS-----EALSLKQKIT-----KE 806  
 QY 107 EEDFRKQLEDESGRAKAKENTTAELTEELNKMLLYEELYNKTKPQIOLDAFEVEKQAL 166  
 Db 807 EE---KQILKQDPETLSQET-----KIOHEELNNRIQTVTTELQVKMEKEAL 851  
 QY 167 LNEHGAQOLNKIRDSY-----AKLLGHQNKOKIKHVKKLKDENSQK 211  
 Db 852 MTELSTVVKDLKSLVSDSLNKSSEFEKNGKRAILDEKTEKELKHOLQVOMENT-LK 910  
 QY 212 SEVSKRLQCLAKKQSETKLOEELNKV 238  
 Db 911 -FOKELKSLKEKEKESHOLKLELNSM 936

## RESULT 14

ID Q44929 PRELIMINARY; PRT: 1690 AA.  
 AC Q44929;  
 DT 01-JUN-1998 (TREMblrel. 06, Created)  
 DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)  
 DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 GN Microtubule binding protein D-CLIP-190.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxId=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-OREGON R.  
 RA Lantz V.A., Miller K.G.,  
 RL J. Cell Biol. 0:0-0(1998).  
 DR EMBL: AF041382; AAB96783.1;  
 DR Flybase: FBgn020503; CLIP-190.  
 DR InterPro: IPR000938; CAP-Gly.  
 DR Pfam: PF01302; CAP\_GLY; 2.  
 SQ SEQUENCE 1690 AA; 189103 MW; BE4F48FD15F17A7C CRC64;

Query Match 15.9%; Score 190; DB 5; Length 1690;  
 Best Local Similarity 27.1%; Pred. No. 0.057;  
 Matches 75; Conservative 53; Mismatches 107; Indels 42; Gaps 11;

QY 2 EKYSMVQSLQEDVTAQFESYKALTYSEIDKLKLENSLOEKAA---KAGNAEDVOHQIL 58  
 Db 629 EOIRELNQOLDEVYTTQNLVOKKADSDMLRIQKEGTEKSTLLEKTELVQIKEQA 688  
 QY 59 ATSSNOEYRMLDLOTKSALKETKEITVSELOKTTDLONLQKQ-EDR 111  
 Db 689 KITLODKQOLKQISDLK-QLAEQEKLVREKTENAINQIOLEKESIQOLALKQNELEDRQ 747  
 QY 112 KQLEDEGR---KAKEKNTTAEITFEINKRWLYEELYNKT---KPPQIOLDAFEVEKQ 164  
 Db 748 KQSESEVHQLQELKQNTQKDELVESEGSGLKLOOLLEKTLGHKILQAALEELKKE 807  
 QY 165 ALNENGAQOOL-NKIRDSYAKL-----LGHONLQKTI-----KHVYKLDENSQK 211  
 Db 808 TIRKEEOELQOLQSKSASESALKVYVOLBOLOQQAASGESEKTVAKLHDELQK 867  
 QY 212 SEVSKRLQCLAKKQSETKLOEELNKV 237  
 Db 868 SQAEETQSELKSTESNLEKSKOLEANGLSEBEAKK 904

## RESULT 15

ID Q9DGM4 PRELIMINARY; PRT: 1941 AA.  
 AC Q9DGM4;  
 DT 01-MAR-2001 (TREMblrel. 16, Created)  
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE Fast myosin heavy chain-isoform 3.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxId=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang Q., Bandman E.;  
 RT "Seven skeletal myosin heavy chain genes (MyHC) are organized as a  
 multigene complex in the chicken genome.";  
 RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF272034; AAF9315.1;  
 DR HSSP: P13538; 2MYS.  
 DR InterPro: IPR000048; IQ\_region.  
 DR InterPro: IPR001609; myosin\_head.  
 DR InterPro: IPR004009; myosin\_N.  
 DR InterPro: IPR002928; myosin\_tail.  
 DR InterPro: IPR000533; Tropomyosin.  
 DR Pfam: PF00612; IQ; 2.  
 DR Pfam: PF00063; myosin\_head; 1.  
 DR Pfam: PF02736; myosin\_N; 1.  
 DR Pfam: PF01576; myosin\_tail; 1.  
 DR PRINTS: PR00193; MYOSTINHEAVY.  
 DR PRINTS: PR00194; TROPOMYSIN.  
 DR Prodom: PD000355; myosin\_head; 1.  
 DR SMART: SM00015; IQ; 1.  
 DR SMART: SM00242; MYSC; 1.  
 SQ SEQUENCE 1941 AA; 223162 MW; 9C8597C1CFCFIDBEC CRC64;

Query Match 15.9%; Score 189.5; DB 13; Length 1941;  
Best Local Similarity 21.1%; Pred. NO.0.069;  
Matches 75; Conservative 53; Mismatches 107; Indels 121; Gaps 9;

QY 8 VOSLEDVTAOFESYKALTASEIEDLKLNSLQEKAKAGKNADVOHOILATFESSNOEY 67  
DB 1212 IDNQRVKOKLEKEKSELKMEIDDLASNMESVSNAKANLEKMCRTLEDQLEIKTEEH 1271  
QY 68 VRLLDLQTSALKETEIKEIT-----VSFLQKITDLONLKOQ----- 106  
DB 1272 QRMINDLNTQARLQTEAGEYSRQVEEKDALISLRSKGAFQOIEELKRHLEELIKAK 1331  
QY 107 -----EED---FRKLEDEBGRKAKENTTAELTEINKWLLY-----EEL 145  
DB 1332 NALAHALQSRHDCDLREQYEEQEKGLQALSKANSEVAQWRTKYETDAIQRTPEEL 1391  
QY 146 YNKTKEPFOQLD-----AFEYKQALLNE-----HGAQOQLNKIR 181  
DB 1392 EEAKKKLAQRLQDAEHEHVEAVNAKASLEKTKQRLONEVEDLMIDIVERANACALDKQ 1451  
QY 182 DSYAKLLGHONLK-----OKIKHVVKLKDENSOLK 211  
DB 1452 KNPDKTLAEKKQYEEETOAELEASOKESRSISTELFKMKNAVPEESLDHLOTLKREKNLQ 1511  
QY 212 SEVSKLRCOLAK-----KKQ-----SETKLOELNKVIGIK 242  
DB 1512 QEISDLTEQIAEGKAIHELEKVKKOIEQEKSEIOALEEAEASLEHEGKILRLQ 1567

Search completed: July 17, 2003, 16:10:09  
Job time : 34 secs

